

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/554,561
Source: PJT/10
Date Processed by STIC: 11/3/05

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 11/03/2005

PATENT APPLICATION: US/10/554,561

TIME: 08:31:03

Input Set : A:\082368-006600US.txt

Output Set: N:\CRF4\11032005\J554561.raw

```

4 <110> APPLICANT: Ebina, Yousuke
5      Obata, Toshiyuki
6      Okamoto, Eiji
8 <120> TITLE OF INVENTION: METHODS FOR MEASURING THE INSULIN
9      RECEPTOR ALPHA SUBUNIT
11 <130> FILE REFERENCE: 082368-006600US
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/554,561
C--> 13 <141> CURRENT FILING DATE: 2005-10-25
13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/005412
14 <151> PRIOR FILING DATE: 2004-04-15
16 <150> PRIOR APPLICATION NUMBER: JP 2003-121955
17 <151> PRIOR FILING DATE: 2003-04-25
19 <150> PRIOR APPLICATION NUMBER: JP 2003-433303
20 <151> PRIOR FILING DATE: 2003-12-26
22 <160> NUMBER OF SEQ ID NOS: 2
24 <170> SOFTWARE: FastSEQ for Windows Version 4.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 2859
28 <212> TYPE: DNA
29 <213> ORGANISM: Homo sapiens
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33 <222> LOCATION: (1)...(81)
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (1)...(2859)
W--> 38 <221> mat_peptide
39 <222> LOCATION: (82)...(926)
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43 Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
44      -25      -20      -15
46 gcg gtg gcc gcg ctg cta ctg ggc gcc gcg ggc cac ctg tac ccc gga 96
47 Ala Val Ala Ala Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly
48      -10      -5      1      5
50 gag gtg tgt ccc ggc atg gat atc cgg aac aac ctc act agg ttg cat 144
51 Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His
52      10      15      20
54 gag ctg gag aat tgc tct gtc atc gaa gga cac ttg cag ata ctc ttg 192
55 Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu
56      25      30      35
58 atg ttc aaa acg agg ccc gaa gat ttc cga gac ctc agt ttc ccc aaa 240
59 Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys
60      40      45      50

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62 ctc atc atg atc act gat tac ttg ctg ctc ttc cgg gtc tat ggg ctc 288
63 Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu
64 55 60 65
66 gag agc ctg aag gac ctg ttc ccc aac ctc acg gtc atc cgg gga tca 336
67 Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser
68 70 75 80 85
70 cga ctg ttc ttt aac tac gcg ctg gtc atc ttc gag atg gtt cac ctc 384
71 Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu
72 90 95 100
74 aag gaa ctc ggc ctc tac aac ctg atg aac atc acc cgg ggt tct gtc 432
75 Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val
76 105 110 115
78 cgc atc gag aag aac aat gag ctc tgt tac ttg gcc act atc gac tgg 480
79 Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp
80 120 125 130
82 tcc cgt atc ctg gat tcc gtg gag gat aat cac atc gtg ttg aac aaa 528
83 Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys
84 135 140 145
86 gat gac aac gag gag tgt gga gac atc tgt ccg ggt acc gcg aag ggc 576
87 Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly
88 150 155 160 165
90 aag acc aac tgc ccc gcc acc gtc atc aac ggg cag ttt gtc gaa cga 624
91 Lys Thr Asn Cys Pro Ala Thr Val Ile Asn Gly Gln Phe Val Glu Arg
92 170 175 180
94 tgt tgg act cat agt cac tgc cag aaa gtt tgc ccg acc atc tgt aag 672
95 Cys Trp Thr His Ser His Cys Gln Lys Val Cys Pro Thr Ile Cys Lys
96 185 190 195
98 tca cac ggc tgc acc gcc gaa ggc ctc tgt tgc cac agc gag tgc ctg 720
99 Ser His Gly Cys Thr Ala Glu Gly Leu Cys Cys His Ser Glu Cys Leu
100 200 205 210
102 ggc aac tgt tct cag ccc gac gac ccc acc aag tgc gtg gcc tgc cgc 768
103 Gly Asn Cys Ser Gln Pro Asp Asp Pro Thr Lys Cys Val Ala Cys Arg
104 215 220 225
106 aac ttc tac ctg gac ggc agg tgt gtg gag acc tgc ccg ccc ccg tac 816
107 Asn Phe Tyr Leu Asp Gly Arg Cys Val Glu Thr Cys Pro Pro Pro Tyr
108 230 235 240 245
110 tac cac ttc cag gac tgg cgc tgt gtg aac ttc agc ttc tgc cag gac 864
111 Tyr His Phe Gln Asp Trp Arg Cys Val Asn Phe Ser Phe Cys Gln Asp
112 250 255 260
114 ctg cac cac aaa tgc aag aac tcg cgg agg cag ggc tgc cac caa tac 912
115 Leu His His Lys Cys Lys Asn Ser Arg Arg Gln Gly Cys His Gln Tyr
116 265 270 275
118 gtc att cac aac aac aag tgc atc cct gag tgt ccc tcc ggg tac acg 960
119 Val Ile His Asn Asn Lys Cys Ile Pro Glu Cys Pro Ser Gly Tyr Thr
120 280 285 290
122 atg aat tcc agc aac ttg ctg tgc acc cca tgc ctg ggt ccc tgt ccc 1008
123 Met Asn Ser Ser Asn Leu Leu Cys Thr Pro Cys Leu Gly Pro Cys Pro
124 295 300 305
126 aag gtg tgc cac ctc cta gaa ggc gag aag acc atc gac tcg gtg acg 1056

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127	Lys	Val	Cys	His	Leu	Leu	Glu	Gly	Glu	Lys	Thr	Ile	Asp	Ser	Val	Thr	
128	310						315				320					325	
130	tct	gcc	cag	gag	ctc	cga	gga	tgc	acc	gtc	atc	aac	ggg	agt	ctg	atc	1104
131	Ser	Ala	Gln	Glu	Leu	Arg	Gly	Cys	Thr	Val	Ile	Asn	Gly	Ser	Leu	Ile	
132					330					335					340		
134	atc	aac	att	cga	gga	ggc	aac	aat	ctg	gca	gct	gag	cta	gaa	gcc	aac	1152
135	Ile	Asn	Ile	Arg	Gly	Gly	Asn	Asn	Leu	Ala	Ala	Glu	Leu	Glu	Ala	Asn	
136				345					350					355			
138	ctc	ggc	ctc	att	gaa	gaa	att	tca	ggg	tat	cta	aaa	atc	cgc	cga	tcc	1200
139	Leu	Gly	Leu	Ile	Glu	Glu	Ile	Ser	Gly	Tyr	Leu	Lys	Ile	Arg	Arg	Ser	
140			360						365					370			
142	tac	gct	ctg	gtg	tca	ctt	tcc	ttc	ttc	cgg	aag	tta	cgt	ctg	att	cga	1248
143	Tyr	Ala	Leu	Val	Ser	Leu	Ser	Phe	Phe	Arg	Lys	Leu	Arg	Leu	Ile	Arg	
144			375						380					385			
146	gga	gag	acc	ttg	gaa	att	ggg	aac	tac	tcc	ttc	tat	gcc	ttg	gac	aac	1296
147	Gly	Glu	Thr	Leu	Glu	Ile	Gly	Asn	Tyr	Ser	Phe	Tyr	Ala	Leu	Asp	Asn	
148	390					395					400				405		
150	cag	aac	cta	agg	cag	ctc	tgg	gac	tgg	agc	aaa	cac	aac	ctc	acc	acc	1344
151	Gln	Asn	Leu	Arg	Gln	Leu	Trp	Asp	Trp	Ser	Lys	His	Asn	Leu	Thr	Thr	
152				410						415					420		
154	act	cag	ggg	aaa	ctc	ttc	ttc	cac	tat	aac	ccc	aaa	ctc	tgc	ttg	tca	1392
155	Thr	Gln	Gly	Lys	Leu	Phe	Phe	His	Tyr	Asn	Pro	Lys	Leu	Cys	Leu	Ser	
156				425						430					435		
158	gaa	atc	cac	aag	atg	gaa	gaa	gtt	tca	gga	acc	aag	ggg	cgc	cag	gag	1440
159	Glu	Ile	His	Lys	Met	Glu	Glu	Val	Ser	Gly	Thr	Lys	Gly	Arg	Gln	Glu	
160			440						445					450			
162	aga	aac	gac	att	gcc	ctg	aag	acc	aat	ggg	gac	aag	gca	tcc	tgt	gaa	1488
163	Arg	Asn	Asp	Ile	Ala	Leu	Lys	Thr	Asn	Gly	Asp	Lys	Ala	Ser	Cys	Glu	
164			455				460						465				
166	aat	gag	tta	ctt	aaa	ttt	tct	tac	att	cgg	aca	tct	ttt	gac	aag	atc	1536
167	Asn	Glu	Leu	Leu	Lys	Phe	Ser	Tyr	Ile	Arg	Thr	Ser	Phe	Asp	Lys	Ile	
168	470					475					480				485		
170	ttg	ctg	aga	tgg	gag	ccg	tac	tgg	ccc	ccc	gac	ttc	cga	gac	ctc	ttg	1584
171	Leu	Leu	Arg	Trp	Glu	Pro	Tyr	Trp	Pro	Pro	Asp	Phe	Arg	Asp	Leu	Leu	
172				490						495					500		
174	ggg	ttc	atg	ctg	ttc	tac	aaa	gag	gcc	cct	tat	cag	aat	gtg	acg	gag	1632
175	Gly	Phe	Met	Leu	Phe	Tyr	Lys	Glu	Ala	Pro	Tyr	Gln	Asn	Val	Thr	Glu	
176				505						510					515		
178	ttc	gat	ggg	cag	gat	gcg	tgt	ggt	tcc	aac	agt	tgg	acg	gtg	gta	gac	1680
179	Phe	Asp	Gly	Gln	Asp	Ala	Cys	Gly	Ser	Asn	Ser	Trp	Thr	Val	Val	Asp	
180			520						525					530			
182	att	gac	cca	ccc	ctg	agg	tcc	aac	gac	ccc	aaa	tca	cag	aac	cac	cca	1728
183	Ile	Asp	Pro	Pro	Leu	Arg	Ser	Asn	Asp	Pro	Lys	Ser	Gln	Asn	His	Pro	
184			535				540					545					
186	ggg	tgg	ctg	atg	cgg	ggt	ctc	aag	ccc	tgg	acc	cag	tat	gcc	atc	ttt	1776
187	Gly	Trp	Leu	Met	Arg	Gly	Leu	Lys	Pro	Trp	Thr	Gln	Tyr	Ala	Ile	Phe	
188	550					555					560				565		
190	gtg	aag	acc	ctg	gtc	acc	ttt	tcg	gat	gaa	cgc	cgg	acc	tat	ggg	gcc	1824
191	Val	Lys	Thr	Leu	Val	Thr	Phe	Ser	Asp	Glu	Arg	Arg	Thr	Tyr	Gly	Ala	

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192		570		575		580		
194	aag agt gac atc att tat gtc cag aca gat gcc acc aac ccc tct gtg	1872						
195	Lys Ser Asp Ile Ile Tyr Val Gln Thr Asp Ala Thr Asn Pro Ser Val							
196		585		590		595		
198	ccc ctg gat cca atc tca gtg tct aac tca tca tcc cag att att ctg	1920						
199	Pro Leu Asp Pro Ile Ser Val Ser Asn Ser Ser Ser Gln Ile Ile Leu							
200		600		605		610		
202	aag tgg aaa cca ccc tcc gac ccc aat ggc aac atc acc cac tac ctg	1968						
203	Lys Trp Lys Pro Pro Ser Asp Pro Asn Gly Asn Ile Thr His Tyr Leu							
204		615		620		625		
206	gtt ttc tgg gag agg cag gcg gaa gac agt gag ctg ttc gag ctg gat	2016						
207	Val Phe Trp Glu Arg Gln Ala Glu Asp Ser Glu Leu Phe Glu Leu Asp							
208	630		635		640		645	
210	tat tgc ctc aaa ggg ctg aag ctg ccc tcg agg acc tgg tct cca cca	2064						
211	Tyr Cys Leu Lys Gly Leu Lys Leu Pro Ser Arg Thr Trp Ser Pro Pro							
212		650		655		660		
214	ttc gag tct gaa gat tct cag aag cac aac cag agt gag tat gag gat	2112						
215	Phe Glu Ser Glu Asp Ser Gln Lys His Asn Gln Ser Glu Tyr Glu Asp							
216		665		670		675		
218	tcg gcc ggc gaa tgc tgc tcc tgt cca aag aca gac tct cag atc ctg	2160						
219	Ser Ala Gly Glu Cys Cys Ser Cys Pro Lys Thr Asp Ser Gln Ile Leu							
220		680		685		690		
222	aag gag ctg gag gag tcc tcg ttt agg aag acg ttt gag gat tac ctg	2208						
223	Lys Glu Leu Glu Glu Ser Ser Phe Arg Lys Thr Phe Glu Asp Tyr Leu							
224		695		700		705		
226	cac aac gtg gtt ttc gtc ccc aga aaa acc tct tca ggc act ggt gcc	2256						
228	His Asn Val Val Phe Val Pro Arg Lys Thr Ser Ser Gly Thr Gly Ala							
229	710		715		720		725	
231	gag gac cct agg cca tct cgg aaa cgc agg tcc ctt ggc gat gtt ggg	2304						
232	Glu Asp Pro Arg Pro Ser Arg Lys Arg Arg Ser Leu Gly Asp Val Gly							
233		730		735		740		
235	aat gtg acg gtg gcc gtg ccc acg gtg gca gct ttc ccc aac act tcc	2352						
236	Asn Val Thr Val Ala Val Pro Thr Val Ala Ala Phe Pro Asn Thr Ser							
237		745		750		755		
239	tcg acc agc gtg ccc acg agt ccg gag gag cac agg cct ttt gag aag	2400						
240	Ser Thr Ser Val Pro Thr Ser Pro Glu Glu His Arg Pro Phe Glu Lys							
241		760		765		770		
243	gtg gtg aac aag gag tcg ctg gtc atc tcc ggc ttg cga cac ttc acg	2448						
244	Val Val Asn Lys Glu Ser Leu Val Ile Ser Gly Leu Arg His Phe Thr							
245		775		780		785		
247	ggc tat cgc atc gag ctg cag gct tgc aac cag gac acc cct gag gaa	2496						
248	Gly Tyr Arg Ile Glu Leu Gln Ala Cys Asn Gln Asp Thr Pro Glu Glu							
249	790		795		800		805	
251	cgg tgc agt gtg gca gcc tac gtc agt gcg agg acc atg cct gaa gcc	2544						
252	Arg Cys Ser Val Ala Ala Tyr Val Ser Ala Arg Thr Met Pro Glu Ala							
253		810		815		820		
255	aag gct gat gac att gtt ggc cct gtg acg cat gaa atc ttt gag aac	2592						
256	Lys Ala Asp Asp Ile Val Gly Pro Val Thr His Glu Ile Phe Glu Asn							
257		825		830		835		

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259 aac gtc gtc cac ttg atg tgg cag gag ccg aag gag ccc aat ggt ctg      2640
260 Asn Val Val His Leu Met Trp Gln Glu Pro Lys Glu Pro Asn Gly Leu
261      840      845      850
263 atc gtg ctg tat gaa gtg agt tat cgg cga tat ggt gat gag gag ctg      2688
264 Ile Val Leu Tyr Glu Val Ser Tyr Arg Arg Tyr Gly Asp Glu Glu Leu
265      855      860      865
267 cat ctc tgc gtc tcc cgc aag cac ttc gct ctg gaa cgg ggc tgc agg      2736
268 His Leu Cys Val Ser Arg Lys His Phe Ala Leu Glu Arg Gly Cys Arg
269 870      875      880      885
271 ctg cgt ggg ctg tca ccg ggg aac tac agc gtg cga atc cgg gcc acc      2784
272 Leu Arg Gly Leu Ser Pro Gly Asn Tyr Ser Val Arg Ile Arg Ala Thr
273      890      895      900
276 tcc ctt gcg ggc aac ggc tct tgg acg gaa ccc acc tat ttc tac gtg      2832
277 Ser Leu Ala Gly Asn Gly Ser Trp Thr Glu Pro Thr Tyr Phe Tyr Val
278      905      910      915
280 aca gac tat tta gac gtc ccg tca aat      2859
281 Thr Asp Tyr Leu Asp Val Pro Ser Asn
282      920      925
285 <210> SEQ ID NO: 2
286 <211> LENGTH: 953
287 <212> TYPE: PRT
288 <213> ORGANISM: Homo sapiens
290 <220> FEATURE:
291 <221> NAME/KEY: SIGNAL
292 <222> LOCATION: (1)...(27)
294 <400> SEQUENCE: 2
295 Met Gly Thr Gly Gly Arg Arg Gly Ala Ala Ala Ala Pro Leu Leu Val
296      -25      -20      -15
297 Ala Val Ala Ala Leu Leu Leu Gly Ala Ala Gly His Leu Tyr Pro Gly
298      -10      -5      1      5
299 Glu Val Cys Pro Gly Met Asp Ile Arg Asn Asn Leu Thr Arg Leu His
300      10      15      20
301 Glu Leu Glu Asn Cys Ser Val Ile Glu Gly His Leu Gln Ile Leu Leu
302      25      30      35
303 Met Phe Lys Thr Arg Pro Glu Asp Phe Arg Asp Leu Ser Phe Pro Lys
304      40      45      50
305 Leu Ile Met Ile Thr Asp Tyr Leu Leu Leu Phe Arg Val Tyr Gly Leu
306      55      60      65
307 Glu Ser Leu Lys Asp Leu Phe Pro Asn Leu Thr Val Ile Arg Gly Ser
308 70      75      80      85
309 Arg Leu Phe Phe Asn Tyr Ala Leu Val Ile Phe Glu Met Val His Leu
310      90      95      100
311 Lys Glu Leu Gly Leu Tyr Asn Leu Met Asn Ile Thr Arg Gly Ser Val
312      105      110      115
313 Arg Ile Glu Lys Asn Asn Glu Leu Cys Tyr Leu Ala Thr Ile Asp Trp
314      120      125      130
315 Ser Arg Ile Leu Asp Ser Val Glu Asp Asn His Ile Val Leu Asn Lys
316      135      140      145
317 Asp Asp Asn Glu Glu Cys Gly Asp Ile Cys Pro Gly Thr Ala Lys Gly

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:38 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1

L:41 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1